

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Mc Wherter, Charles
Feng, Yiqing
Mc Kearn, John
Staten, Nicholas
Streeter, Philip
Woulfe, Susan
Minster, Nancy
Minnerly, John
- (ii) TITLE OF THE INVENTION: Circular Permuteins of FLT3 Ligand
- (iii) NUMBER OF SEQUENCES: 151
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Carol M. Nielsen, Gardere Wynne Sewell LLP
 - (B) STREET: 1000 Louisiana, Suite 3400
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: USA
 - (F) ZIP: 77002
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: CD
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Unknown
 - (B) FILING DATE: 20-AUG-2003
 - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/955,090
 - (B) FILING DATE: 21-OCT-97
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/030,094
 - (B) FILING DATE: 25-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Nielsen, Carol M.
 - (B) REGISTRATION NUMBER: 37,676
 - (C) REFERENCE/DOCKET NUMBER: 126181-1059
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 713-276-5383
 - (B) TELEFAX: 713-276-5555
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Ala	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55				60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70					75					80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
	130					135									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55				60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70					75					80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	

Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
		20						25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35				40						45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55					60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70					75					80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val
				85					90					95	
Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu
			100					105					110		
Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu						
	115						120								

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
		20						25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35				40						45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55					60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile

65					70					75					80
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
	130					135									

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55				60					
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70				75					80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		

Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35					40					45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55					60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70					75				80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro									
	130					135									

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe
1				5					10					15	
Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro
			20					25					30		
Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu
		35				40						45			
Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val
	50					55					60				
Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile
65					70					75				80	
His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg
				85					90					95	
Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln
			100					105					110		
Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys
		115					120					125			
Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75				80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Ser
			100					105					110		
Gly	Gly	Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
		115					120					125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
	130					135					140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145					150				155						

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35					40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75				80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Thr
			100					105					110		
Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val
		115					120					125			
Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr
	130					135					140				
Val	Ala	Ser	Asn	Leu	Gln										
145					150										

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			35				40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55				60					
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70				75					80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90					95		
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe
			100					105					110		
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
		115					120					125			
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
	130					135					140				
Gln															
145															

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
1				5				10						15	
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
			20					25					30		
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
			35				40					45			
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
	50					55				60					
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly
65					70					75				80	
Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe
			85					90					95		
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
			100					105					110		

Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
		115					120					125			
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
		130				135					140				
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
1				5					10				15		
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
			20					25				30			
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
		35					40					45			
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
	50					55				60					
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly
65				70					75					80	
Ser	Gly	Gly	Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile
			85					90					95		
Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu
			100					105				110			
Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu
		115					120					125			
Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg
	130					135					140				
Leu	Lys	Thr	Val	Ala	Gly										
145					150										

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
1				5					10				15		
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
			20					25				30			
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu

		35					40					45							
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu				
	50					55					60								
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly				
65					70					75				80					
Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala				
				85					90					95					
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val				
			100					105					110						
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp				
	115						120					125							
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala				
	130					135					140								
Gly																			
145																			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu				
1				5					10					15					
Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr				
			20					25					30						
Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser				
		35				40					45								
Ser	Thr	Leu	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly	Asn	Gly	Ser	Gly	Gly				
	50					55					60								
Asn	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp				
65				70						75				80					
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr				
				85					90					95					
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly				
			100					105					110						
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr				
	115						120					125							
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu				
	130					135					140								
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro									
145					150					155									

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

(2) INFORMATION FOR SEQ ID NO:16:

(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

[illegible]

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			35				40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
50						55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75				80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90						95	
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Ser
			100					105					110		
Gly	Gly	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
			115				120					125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
			130				135				140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145						150				155					

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			35				40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
50						55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75				80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro

				85					90					95			
Asp	Ser	Ser	Thr	Leu	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Thr		
			100					105					110				
Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val		
		115					120					125					
Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr		
		130				135					140						
Val	Ala	Ser	Asn	Leu	Gln												
145					150												

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp		
1				5				10					15				
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr		
			20					25					30				
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly		
		35				40						45					
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr		
	50					55				60							
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu		
65				70						75				80			
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu		
			85						90				95				
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu		
			100					105					110				
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg		
		115					120					125					
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly		
		130				135					140						
Ser																	
145																	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly	Ser	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser		
1				5					10					15			

Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
			20					25					30		
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys
		35					40					45			
Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu
	50					55					60				
Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn
65					70					75					80
Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser
				85					90					95	
Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr
			100					105					110		
Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe
		115					120					125			
Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
1				5					10					15	
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
			20					25					30		
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
		35				40						45			
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
	50					55					60				
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
65					70					75					80
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu
				85					90					95	
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu
			100					105					110		
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg
		115					120					125			
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly
	130					135					140				
Ser	Gly	Gly	Gly	Ser											
145															

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Gln	Asp	Cys	Ser	
1				5				10						15		
Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	
			20					25					30			
Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	
		35					40					45				
Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	
	50					55					60					
Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	
65					70					75					80	
Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	
				85					90					95		
Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	
			100					105						110		
Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	
		115					120					125				
Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	
	130					135					140					
Pro	Asp	Ser	Ser	Thr	Leu											
145					150											

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	
1				5				10						15		
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	
			20					25					30			
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	
		35					40					45				
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	
	50					55					60					
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	
65					70				75						80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	
				85					90					95		

Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Thr	Gln	Asp	Cys	Ser
			100					105					110		
Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu
		115					120					125			
Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn
	130					135					140				
Leu	Gln														
145															

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10					15		
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20				25					30			
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
		35				40					45				
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55				60					
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65				70				75						80	
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
			85				90					95			
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys
			100				105					110			
Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg
		115				120					125				
Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser
	130					135					140				
Asn	Leu	Gln													
145															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10					15		
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			35				40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75					80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90						95	
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			100					105					110		
Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser
		115					120					125			
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
	130					135					140				
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1				5				10						15	
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20					25					30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
			35				40					45			
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50					55					60				
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65					70					75					80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
				85				90						95	
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly
			100					105					110		
Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe
		115					120					125			
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
	130					135					140				

Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
145					150					155					160
Gln															

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu
1				5					10					15	
Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg
			20					25					30		
Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val
		35					40					45			
Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro
	50					55					60				
Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu
65					70				75					80	
Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn
				85				90						95	
Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu
			100					105					110		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr
		115					120					125			
Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val
	130					135					140				
Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg
1				5					10					15	
Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly
			20					25					30		
Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe
		35					40					45			
Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val

50		55		60
Gln Thr Asn Ile Ser Arg	Leu Leu Gln Glu Thr	Ser Glu Gln Leu Val		
65	70	75	80	
Ala Leu Lys Pro Trp	Ile Thr Arg Gln Asn Phe	Ser Arg Cys Leu Glu		
	85	90	95	
Leu Gln Cys Gln Pro Asp	Ser Ser Thr Leu Gly Gly Gly	Ser Gly Gly		
	100	105	110	
Gly Ser Gly Gly Gly Ser	Gly Gly Thr Gln Asp Cys	Ser Phe Gln		
	115	120	125	
His Ser Pro Ile Ser Ser	Asp Phe Ala Val Lys	Ile Arg Glu Leu Ser		
	130	135	140	
Asp Tyr Leu Leu Gln Asp	Tyr Pro Val Thr Val			
145	150	155		

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr	
1	15
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys	
	30
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser	
	45
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser	
	60
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly	
	75
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Thr Gln Asp	
	90
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile	
	110
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala	
	125
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val	
	140
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr	
145	155

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
1				5				10					15		
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
			20					25					30		
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
			35					40					45		
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
	50						55				60				
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly
65					70					75					80
Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe
				85					90					95	
Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu
			100					105					110		
Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu
			115					120					125		
Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
	130						135					140			
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu
1				5				10					15		
Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr
			20					25					30		
Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser
			35					40					45		
Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly
	50					55					60				
Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
65					70					75					80
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
			85						90					95	
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
			100					105					110		
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
			115					120					125		
Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
	130						135					140			
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser
1				5				10						15	
Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser
			20					25					30		
Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly
		35					40					45			
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp
	50					55				60					
Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile
65					70					75					80
Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala
			85						90					95	
Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val
			100					105					110		
Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys
		115					120					125			
Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr
	130					135					140				
Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val
1				5				10						15	
Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu
			20					25					30		
Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly
		35					40					45			
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln
	50					55					60				
His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser
65				70						75					80
Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln
			85					90					95		
Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg

				100					105					110			
Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu		
		115					120					125					
Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe		
	130					135					140						
Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln							
145					150					155							

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Ser

1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Gly Gly Ser Gly Gly Gly Ser

7

5

(2) INFORMATION FOR SEO ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Gly Ser Gly Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Phe Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Phe Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Phe Gly Gly Asn Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Ser Asp Met Ala Gly
1 .5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Gly Gly Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Gly Ser Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Gly Ser Gly Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15
Gly Gly Gly Ser Gly
20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGACCATGG CNACCCAGGA CTGCTCCTTC CAA 33

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACTGAAGCTT AGGGCTGACA CTGCAGCTCC AG 32

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTGAAGCTT ACAGGGTTGA GGAGTCGGGC TG 32

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC 46

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC 46

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGTCCAAACT CATCAATGTA TC 22

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGCCATG GCCGACGAGG AGCTCTGCGG GGGCCTCT 38

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTAGAAGCT TACTGCAGGT TGGAGGCCAC GGTGAC 36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CATGGCCATG GCCTCCAAGA TGCAAGGCTT GCTGGAGC 38

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAGAAGCT TACCCAGCGA CAGTCTTGAG CCGCTC 36

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CATGGCCATG GCCCCCCCCA GCTGTCTTCG CTTCGT 36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTAGAAGCT TAGGGCTGAA AGGCACATTT GGTGACA 37

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCCTGTCTGG CGGCAACGGC ACCCAGGACT GCTCCTTCCA AC 42

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCGGTAACGG CAGTGGAGGT AATGGCACCC AGGACTGCTC CTTCCAAC 48

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACGGCAGTGG TGGCAATGGG AGCGGCGGAA ATGGAACCCA GGACTGCTCC TTCCAAC 57

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGCCGTTGC CGCCAGACAG GGTGAGGAG TCGGGCTG 38

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTACCTCCA CTGCCGTTAC CGCCTGACAG GGTGAGGAG TCGGGCTG 48

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCTCCCATTG CCACCACTGC CGTTACCTCC AGACAGGGTT GAGGAGTCGG GCTG 54

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATGAGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC TCCTTCCACC 60

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GATGACGGAT CCGTTACCTC CAGACAGGGT TGAGGAGTCG GGCTG 45

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATGACGGAT CCGGAGGTAA TGGCACCCAG GACTGCTCCT TCCAAC 46

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GACTGCCATG GCCGACGAGG AGCTCTGCG 29

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GACTCAAGCT TACTGCAGGT TGGAGGCC 28

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GACTCGGGAT CCGGAGGTTC TGGCACCCAG GACTGCTCC 39

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GACTGGGATC CGGTGGCAGT GGGAGCGGCG GATCTGGAAC C 41

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACTTGGGAT CCACTACCTC CAGACAGGGT TGAGGAGTC 39

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACTGACGGAT CCACCGCCCA GGGTTGAGGA GTCGGGCTG 39

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACTGACGGAT CCACCTCCTG ACCCACCGCC CAGGGTTGAG GAGTCGGGCT G 51

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACTGACGGAT CCACCTCCTG ACCCACCTCC TGACCCACCG CCCAGGGTTG AGGAGTCGGG 60
CTG 63

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACGTAAAGCT TACAGGGTTG AGGAGTCG

28

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCAGTGGAT CCGGAGGTAC CCAGGACTGC TCCTTCCAAC

40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AAC

43

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTCAGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAC

60

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GCGGCTG

57

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC 57

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GTTGCCATGG CNCTGCARGA YGARGARCTG TGYGGYGGCC TCTGGCGGCT GGTCCCTG 57

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGC GGCTGGT CCTGGCA 57

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG 57

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC 57

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG 57

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG 57

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAAGCT TAGGCCACGG TGACTGGGTA 30

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG 30

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC 30

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TATGCAAGCT TACAGGTTGG AGGCCACGGT 30

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGCAAGCT TACTGCAGGT TGGAGGCCAC 30

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TATGCAAGCT TAGTCCTGCA GGTTGGAGGC 30

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TATGCAAGCT TACTCGTCCT GCAGGTTGGA 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TATGCAAGCT TACTCCTCGT CCTGCAGGTT 30

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGC	GCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360

ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	300
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	360
ACCCTG						366

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGAACCTCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGTACCCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360

ACTCGCCAGA ACTTCTCCCG GTGCCTGGAG CTGCAGTGTC AGCCCGACTC CTCAACCCTG 420

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCACTCAGG	ACTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCACTCAGG	ACTGCTCTTT	TCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	420

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTCA	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCTTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAACGGATC	CGGTGGCAAT	GGGAGCGGCG	GAAATGGAAC	CCAGGACTGC	360

TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC TTCGCTGTCA AAATCCGTGA GCTGTCTGAC	420
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAG	465

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTGCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTTCAG CCCCCCCCCA GCTGTCTTCG CTTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGTGAGGCG GTAACGGCAG TGGAGGTAAT GGCACCCAGG ACTGCTCCTT CCAACACAGC	360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT	420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG	450

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTGCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTTCAG CCCCCCCCCA GCTGTCTTCG CTTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGTCTGGCG GCAACGGCAC CCAGGACTGC TCCTTCCAAC ACAGCCCCAT CTCCTCCGAC	360
TTCGCTGTCA AAATCCGTGA GCTGTCTGAC TACCTGCTTC AAGATTACCC AGTCACCGTG	420
GCCTCCAACC TGCAG	435

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA	60
TGTGCCTTTC AGCCCCCCCC CAGCTGTCTT CGCTTCGTCC AGACCAACAT CTCCCGCCTC	120
CTGCAGGAGA CCTCCGAGCA GCTGGTGGCG CTGAAGCCCT GGATCACTCG CCAGAACTTC	180

TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GA CTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGTGGCA	ATGGGAGCGG	CGGAAATGGA	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCTCCG	ACTTCGCTGT	CAAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTGC	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GA CTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGAGGTA	ATGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	300
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	360
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	420
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG				450

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GA CTCCTCAA	CCCTGTCTGG	CGGCAACGGC	240
ACGCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	300
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	360
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	420
AAGACTGTGC	CTGGG					435

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCTGGAG	GTAACGGCAG	TGGTGGCAAT	180
GGGAGCGGTG	GAAATGGAAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCC		465

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCAAGCG	GTAACGGCAG	TGGAGGTAAT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCTTGG	CACAGCGCTG	GATGGAGCGG	360
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	420
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC				450

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGTCTGGCG	GCAACGGCAC	GCAGGACTGC	180
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	240
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	300
GGGGGCCTCT	GGCGGTGGT	CCTGGCACAG	CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	360
GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	420
TGTGCCTTTC	AGCCC					435

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGAGGTTCT	GGCAACCCAG	GACTGCTCCT	TCCAACACAG	360
CCCCATCTCC	TCCGACTTCG	CTGTCAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	420
TTACCCAGTC	ACCGTGGCCT	CCAACCTGCA	G			451

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGTGGCAGT	GGGAGCGGCG	GATCTGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTACACAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGATCC					437

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GGATCCGGAG	GTACCCAGGA	CTGCTCCTTC	CAACACAGCC	CCATCTCCTC	CGACTTCGCT	60
GTCAAAATCC	GTGAGCTGTC	TGACTACCTG	CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	120
AACCTGCAGG	ACGAGGAGCT	CTGCGGGGGC	CTCTGGCGGC	TGGTCCTGGC	ACAGCGCTGG	180
ATGGAGCGGC	TCAAGACTGT	CGCTGGGTCC	AAGATGCAAG	GCTTGCTGGA	GCGCGTGAAC	240
ACGGAGATAC	ACTTTGTCAC	CAAATGTGCC	TTTCAGCCCC	CCCCCAGCTG	TCTTCGCTTC	300
GTCCAGACCA	ACATCTCCCG	CCTCCTGCAG	GAGACCTCCG	AGCAGCTGGT	GGCGCTGAAG	360
CCCTGGATCA	CTCGCCAGAA	CTTCTCCCCG	TGCCTGGAGC	TGCAGTGTCA	GCCCGACTCC	420
TCAACCCTGT	AAGCTT					436

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAATTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGGTCAGGA	GGTGGATCC				449

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCGGAG	GTGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	60
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAAG	ATTACCCAGT	CACCGTGGCC	120
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	180
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG	TCCAAGATGC	AAGGCTTGCT	GGAGCGCGTG	240
AACACGGAGA	TACACTTTGT	CACCAAATGT	GCCTTTCAGC	CCCCCCCCAG	CTGTCTTCGC	300
TTCGTCCAGA	CCAACATCTC	CCGCCTCCTG	CAGGAGACCT	CCGAGCAGCT	GGTGGCGCTG	360
AAGCCCTGGA	TCACTCGCCA	GAACCTTCTC	CGGTGCCTGG	AGCTGCAGTG	TCAGCCCCGAC	420
TCCTCAACCC	TGTAAGCTT					439

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCTGC	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGGTCAGGA	GGTGGGTCAG	GAGGTGGATC	C		461

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGATCCGGAG	GTGGCTCAGG	GGGAGGTAGT	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	60
CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	120
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	180
CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	240
GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	300
CCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	360
GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	420
CTGCAGTGTC	AGCCCGACTC	CTCAACCCTG	TAAGCTT			457

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GATCCGGAGG	TACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	360
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAAGATTA	CCCAGTCACC	420
GTGGCCTCCA	ACCTGCAG					438

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTGCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGGGCGGTG GATCCGGAGG TGGCACCCAG GACTGCTCCT TCCAACACAG CCCCATCTCC	360
TCCGACTTCG CTGTCAAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA TTACCCAGTC	420
ACCGTGGCCT CCAACCTGCA G	441

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTGCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300
CTGGGCGGTG GGTGAGGAGG TGGATCCGGA GGTACCCAGG ACTGCTCCTT CCAACACAGC	360
CCCATCTCCT CCGACTTCGC TGTCAAAATC CGTGAGCTGT CTGACTACCT GCTTCAAGAT	420
TACCCAGTCA CCGTGGCCTC CAACCTGCAG	450

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTGCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACTTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCTCAACC	300

CTGGGCGGTG	GATCCGGAGG	TGGCTCAGGG	GGAGGTAGTG	GTACCCAGGA	CTGCTCCTTC	360
CAACACAGCC	CCATCTCCTC	CGACTTCGCT	GTCAAAATCC	GTGAGCTGTC	TGACTACCTG	420
CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	AACCTGCAG			459

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCTTTTTCAG	CCCCCCCCCA	GCTGCCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	GGTGGATCCG	GAGGTGGCTC	AGGGGGAGGT	360
AGTGGTACCC	AGGACTGCTC	CTTCCAACAC	AGCCCCATCT	CCTCCGACTT	CGCTGTCAAA	420
ATCCGTGAGC	TGTCTGACTA	CCTGCTTCAA	GATTACCCAG	TCACCGTGGC	CTCCAACCTG	480
CAG						483

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCCGATTACC	CAGTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	60
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TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACTGTCGC	TGGGTCCAAG	120
ATGCAAGGCT	TGCTGGAGCG	CGTGAACACG	GAGATACACT	TTGTCACCAA	ATGTGCCTTT	180
CAGCCCCCCC	CCAGCTGTCT	TCGCTTCGTC	CAGACCAACA	TCTCCCGCCT	CCTGCAGGAG	240
ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	300
CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	ACCCTGGGCG	GTGGGTGAGG	AGGTGGGTCA	360
GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	420
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAA		465

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	TGCGGGGGCC	TCTGGCGGCT	GGTCCTGGCA	60
CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	120
CGCGTGAACA	CGGAGATACA	CTTTGTCAAC	AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	180
CTTCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	240
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTGAG	300
CCCGACTCCT	CAACCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	360
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	420
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTG		465

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCCGTGCTG	GGTCCAAGAT	GCAAGGCTTG	CTGGAGCGCG	TGAACACGGA	GATACACTTT	60
GTCACCAAAT	GTGCCTTTCA	GCCCCCCCCC	AGCTGTCTTC	GCTTCGTCCA	GACCAACATC	120
TCCCGCCTCC	TGCAGGAGAC	CTCCGAGCAG	CTGGTGGCGC	TGAAGCCCTG	GATCACTCGC	180
CAGAACTTCT	CCCGGTGCCT	GGAGCTGCAG	TGTCAGCCCG	ACTCCTCAAC	CCTGGGCGGT	240
GGGTGAGGAG	GTGGGTGAGG	AGGTGGATCC	GGAGGTGGCA	CCCAGGACTG	CTCCTTCCAA	300
CACAGCCCCA	TCTCCTCCGA	CTTCGCTGTC	AAAATCCGTG	AGCTGTCTGA	CTACCTGCTT	360
CAAGATTACC	CAGTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	420
TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACT		465

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGGGCGG	TGGGTCAGGA	240
GGTGGGTCAG	GAGGTGGATC	CGGAGGTGGC	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTCT	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGGGCGGTG	GGTCAGGAGG	TGGGTCAGGA	180
GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATACACTT	TGTCACCAAA	TGTGCCTTTC	AGCCC		465

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCCCCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	60
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCTGGAGCT	GCAGTGTGAG	120
CCCGACTCCT	CAACCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCTTGG	CACAGCGCTG	GATGGAGCGG	360
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	420
CACCTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCAGCT	GTCTT		465

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCCACCAACA	TCTCCCGCCT	CCTGCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	60
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTGAGCC	CGACTCCTCA	120
ACCCTGGGCG	GTGGGTCAGG	AGGTGGGTCA	GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	180
TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	240
GACTACCTGC	TTCAAGATTA	CCCAGTCACC	GTGGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	300
TGCGGGGGCC	TCTGGCGGCT	GGTCCTGGCA	CAGCGCTGGA	TGGAGCGGCT	CAAGACTGTC	360
GCTGGGTCCA	AGATGCAAGG	CTTGCTGGAG	CGCGTGAACA	CGGAGATACA	CTTTGTCACC	420
AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	CTTCGCTTCG	TCCAG		465

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	
1				5					10					15		
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	
			20					25					30			
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	
		35					40					45				
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	
	50					55					60					
Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	
65				70					75					80		
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Ser	Cys	Leu	Arg	Phe		
			85					90					95			
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	
		100					105						110			
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	
	115					120						125				
Glu	Leu	Gln	Cys	Gln	Pro											
130																

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala
1				5					10					15	
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val
			20					25					30		
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp
		35					40					45			
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala
	50					55					60				
Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
65					70					75					80
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
				85					90					95	
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
			100						105				110		
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
		115					120					125			
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu					
	130						135								

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala
1				5					10					15	
Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val
			20					25					30		
Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp
		35					40					45			
Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala
	50					55					60				
Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His
65					70					75					80
Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe
				85					90					95	
Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu
			100						105				110		
Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu
		115					120					125			
Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Pro	Pro	Pro	Trp	Ser
	130					135					140				
Pro	Arg	Pro	Leu	Glu	Ala	Thr	Ala	Pro	Thr	Ala	Pro	Gln	Pro	Pro	Leu
145					150					155					160
Leu	Leu	Leu	Leu	Leu	Leu	Pro	Val	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala
				165					170					175	
Trp	Cys	Leu	His	Trp	Gln	Arg	Thr	Arg	Arg	Arg	Thr	Pro	Arg	Pro	Gly
			180				185						190		
Glu	Gln	Val	Pro	Pro	Val	Pro	Ser	Pro	Gln	Asp	Leu	Leu	Leu	Val	Glu
		195					200					205			

His

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTCACCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAGC	CC		402

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTCACCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAGC	CCGACTCCTC	AACCTGCCA	420
CCCCCATGGA	GTCCCCGGCC	CCTGGAGGCC	ACAGCCCCGA	CAGCCCCGCA	GCCCCCTCTG	480
CTCCTCCTAC	TGCTGCTGCC	CGTGGGCCTC	CTGCTGCTGG	CCGCTGCCTG	GTGCCTGCAC	540
TGGCAGAGGA	CGCGGCGGAG	GACACCCCGC	CCTGGGGAGC	AGGTGCCCCC	CGTCCCCAGT	600
CCCCAGGACC	TGCTGCTTGT	GGAGCACTGA				630

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

